

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/510,002  
Source: PCT  
Date Processed by STIC: 01/31/2006

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 01/31/2006

PATENT APPLICATION: US/10/510,002

TIME: 15:38:04

Input Set : E:\G-175US03PCT-SEQLIST.txt

Output Set: N:\CRF4\01312006\J510002.raw

```

3 <110> APPLICANT: Briggs, Kristen
4   Dialynas, Deno
5   Lucas, John
6   Scalia, Aaron
8 <120> TITLE OF INVENTION: XCRF Polynucleotides and Polypeptides and Uses Thereof
10 <130> FILE REFERENCE: WO775
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/510,002
C--> 13 <141> CURRENT FILING DATE: 2004-09-30
15 <160> NUMBER OF SEQ ID NOS: 8
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1297
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (14)...(790)
28 <400> SEQUENCE: 1
29 cgcggggtgtg gtg atg ctg ctg gtg ctg gtg gtg ctc atc ccc gtg ctg      49
30   Met Leu Leu Val Leu Val Val Leu Ile Pro Val Leu
31   1           5           10
33 gtg agc tcg ggc ggc ccg gaa ggc cac tat gag atg ctg ggc acc tgc      97
34 Val Ser Ser Gly Gly Pro Glu Gly His Tyr Glu Met Leu Gly Thr Cys
35   15           20           25
37 cgc atg gtg tgc gac ccc tac ccc gcg cgg ggc ccc ggc gcc ggc gcg      145
38 Arg Met Val Cys Asp Pro Tyr Pro Ala Arg Gly Pro Gly Ala Gly Ala
39   30           35           40
41 cgg acc gac ggc ggc gac gcc ctg agc gag cag agc ggc gcg ccc ccg      193
42 Arg Thr Asp Gly Gly Asp Ala Leu Ser Glu Gln Ser Gly Ala Pro Pro
43 45           50           55           60
45 cct tcc acg ctg gtg cag ggc ccc cag ggg aag ccg ggc cgc acc ggc      241
46 Pro Ser Thr Leu Val Gln Gly Pro Gln Gly Lys Pro Gly Arg Thr Gly
47   65           70           75
49 aag ccc ggc cct ccg ggg cct ccc ggg gac cca ggt cct ccc ggc cct      289
50 Lys Pro Gly Pro Pro Gly Pro Pro Gly Asp Pro Gly Pro Pro Gly Pro
51   80           85           90
53 gtg ggg ccg ccg ggg gag aag ggt gag cca ggc aag ccg ggc cct ccg      337
54 Val Gly Pro Pro Gly Glu Lys Gly Glu Pro Gly Lys Pro Gly Pro Pro
55   95           100          105
57 ggg ctg ccg ggc gcg ggg ggc agc ggc gcc atc agc act gcc acc tac      385
58 Gly Leu Pro Gly Ala Gly Gly Ser Gly Ala Ile Ser Thr Ala Thr Tyr
59 110          115          120
61 acc acg gtg ccg cgc gtg gcc ttc tac gcc ggc ctc aag aac ccc cac      433

```

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62 Thr Thr Val Pro Arg Val Ala Phe Tyr Ala Gly Leu Lys Asn Pro His
63 125 130 135 140
65 gag ggt tac gag gta ctc aag ttt gac gac gtg gtc acc aac cta ggc 481
66 Glu Gly Tyr Glu Val Leu Lys Phe Asp Asp Val Val Thr Asn Leu Gly
67 145 150 155
69 aac aac tac gac gcg gcc agc ggc aag ttt acg tgc aac att ccc ggc 529
70 Asn Asn Tyr Asp Ala Ala Ser Gly Lys Phe Thr Cys Asn Ile Pro Gly
71 160 165 170
73 acc tac ttt ttc acc tac cat gtc ctc atg cgc ggc ggc gac ggc acc 577
74 Thr Tyr Phe Phe Thr Tyr His Val Leu Met Arg Gly Gly Asp Gly Thr
75 175 180 185
77 agt atg tgg gca gac ctc tgc aag aat ggc cag gtg cgg gcc agt gct 625
78 Ser Met Trp Ala Asp Leu Cys Lys Asn Gly Gln Val Arg Ala Ser Ala
79 190 195 200
81 att gcc cag gac gcg gac cag aac tac gac tac gcc agc aac agc gtg 673
82 Ile Ala Gln Asp Ala Asp Gln Asn Tyr Asp Tyr Ala Ser Asn Ser Val
83 205 210 215 220
85 atc ctg cac ctg gac gcc ggc gac gag gtc ttc atc aag ctg gat gga 721
86 Ile Leu His Leu Asp Ala Gly Asp Glu Val Phe Ile Lys Leu Asp Gly
87 225 230 235
89 ggc aaa gca cac ggc ggc aac agc aac aaa tac agc acg ttc tct ggc 769
90 Gly Lys Ala His Gly Gly Asn Ser Asn Lys Tyr Ser Thr Phe Ser Gly
91 240 245 250
93 ttc atc atc tac tcc gac tga gctccccacg tctccctcca cccacgtccc 820
94 Phe Ile Ile Tyr Ser Asp *
95 255
97 tcacccgccg ggggtccctc cgggcggggc agacgatgac tcgcccctcg cccacccgct 880
98 cgctgcccg cctcccccgg ctatgacgcc cccggcccgt gctcaacacc gctgggcca 940
99 cagctaggcc ctcccaccgg ctgctgcag agccgggccc agcgcgccct gtcccctgctc 1000
100 cagggaaccg ggggtgaccg cccccgccca gcccgcgcta tatatttgta caataggact 1060
101 gtttactgcc cacctccgcc tgccagccca cccagcctg gggagagggtc gcggcgccgg 1120
102 gtttgcttcc tgcgctctga gatgagctgc cctccgctcc ctccgggggtg gcgcgcccgg 1180
103 gggagggggg agttgggggc tggatagctt cccagcacc cagagcccc cgccgggctg 1240
104 tgccccgtct gaccaaagtt ataataaaaa cattttcacc ccgcaaaaaa aaaaaaa 1297
106 <210> SEQ ID NO: 2
107 <211> LENGTH: 258
108 <212> TYPE: PRT
109 <213> ORGANISM: Homo sapiens
111 <400> SEQUENCE: 2
112 Met Leu Leu Val Leu Val Val Leu Ile Pro Val Leu Val Ser Ser Gly
113 1 5 10 15
114 Gly Pro Glu Gly His Tyr Glu Met Leu Gly Thr Cys Arg Met Val Cys
115 20 25 30
116 Asp Pro Tyr Pro Ala Arg Gly Pro Gly Ala Gly Ala Arg Thr Asp Gly
117 35 40 45
118 Gly Asp Ala Leu Ser Glu Gln Ser Gly Ala Pro Pro Pro Ser Thr Leu
119 50 55 60
120 Val Gln Gly Pro Gln Gly Lys Pro Gly Arg Thr Gly Lys Pro Gly Pro
121 65 70 75 80

```

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```

122 Pro Gly Pro Pro Gly Asp Pro Gly Pro Pro Gly Pro Val Gly Pro Pro
123      85      90      95
124 Gly Glu Lys Gly Glu Pro Gly Lys Pro Gly Pro Pro Gly Leu Pro Gly
125      100      105      110
126 Ala Gly Gly Ser Gly Ala Ile Ser Thr Ala Thr Tyr Thr Thr Val Pro
127      115      120      125
128 Arg Val Ala Phe Tyr Ala Gly Leu Lys Asn Pro His Glu Gly Tyr Glu
129      130      135      140
130 Val Leu Lys Phe Asp Asp Val Val Thr Asn Leu Gly Asn Asn Tyr Asp
131 145      150      155      160
132 Ala Ala Ser Gly Lys Phe Thr Cys Asn Ile Pro Gly Thr Tyr Phe Phe
133      165      170      175
134 Thr Tyr His Val Leu Met Arg Gly Gly Asp Gly Thr Ser Met Trp Ala
135      180      185      190
136 Asp Leu Cys Lys Asn Gly Gln Val Arg Ala Ser Ala Ile Ala Gln Asp
137      195      200      205
138 Ala Asp Gln Asn Tyr Asp Tyr Ala Ser Asn Ser Val Ile Leu His Leu
139      210      215      220
140 Asp Ala Gly Asp Glu Val Phe Ile Lys Leu Asp Gly Gly Lys Ala His
141 225      230      235      240
142 Gly Gly Asn Ser Asn Lys Tyr Ser Thr Phe Ser Gly Phe Ile Ile Tyr
143      245      250      255
144 Ser Asp
148 <210> SEQ ID NO: 3
149 <211> LENGTH: 864
150 <212> TYPE: DNA
151 <213> ORGANISM: Homo sapiens
153 <220> FEATURE:
154 <221> NAME/KEY: CDS
155 <222> LOCATION: (1)...(864)
157 <400> SEQUENCE: 3
158 atg gca ctg ggg ctg ctg atc gcg gtg cct ctg ctg ctg cag gcg gcg 48
159 Met Ala Leu Gly Leu Leu Ile Ala Val Pro Leu Leu Leu Gln Ala Ala
160 1 5 10 15
162 ccc ccc gga gcg gct cac tac gag atg ctg ggc acc tgc cgc atg atc 96
163 Pro Pro Gly Ala Ala His Tyr Glu Met Leu Gly Thr Cys Arg Met Ile
164 20 25 30
166 tgt gac cca tac agc gtc gct ccc gca ggg gga ccc gcg ggc gcc aag 144
167 Cys Asp Pro Tyr Ser Val Ala Pro Ala Gly Gly Pro Ala Gly Ala Lys
168 35 40 45
170 gct cca ccg ccg gga ccc agt acc gct gcc ctg gaa gtt atg cag gac 192
171 Ala Pro Pro Pro Gly Pro Ser Thr Ala Ala Leu Glu Val Met Gln Asp
172 50 55 60
174 ctc agc gcc aac ccc ccg cct ccg ttt atc cag gga cca aag ggt gat 240
175 Leu Ser Ala Asn Pro Pro Pro Pro Phe Ile Gln Gly Pro Lys Gly Asp
176 65 70 75 80
178 ccg ggg cga cca ggc aag cca ggg cct cgg ggt cct cct gga gag cca 288
179 Pro Gly Arg Pro Gly Lys Pro Gly Pro Arg Gly Pro Pro Gly Glu Pro
180 85 90 95

```

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```

182 ggg cct cct ggg ccc agg ggt ccc ccg gga gag aaa gga gac tcg ggg 336
183 Gly Pro Pro Gly Pro Arg Gly Pro Pro Gly Glu Lys Gly Asp Ser Gly
184 100 105 110
186 agg cca ggg cta ccc gga ctg cag ttg aca acc agc gcg gcc ggt ggc 384
187 Arg Pro Gly Leu Pro Gly Leu Gln Leu Thr Thr Ser Ala Ala Gly Gly
188 115 120 125
190 gtt gga gtg gtg agt ggc gga acc ggg ggc ggt ggc gac acg gag gga 432
191 Val Gly Val Val Ser Gly Gly Thr Gly Gly Gly Asp Thr Glu Gly
192 130 135 140
194 gaa gtg acc agt gcg ctg agc gcc gcc ttc agc ggt ccc aag atc gcc 480
195 Glu Val Thr Ser Ala Leu Ser Ala Ala Phe Ser Gly Pro Lys Ile Ala
196 145 150 155 160
198 ttc tac gtg gga ctc aag agc ccc cac gaa ggc tac gag gtg ctc aag 528
199 Phe Tyr Val Gly Leu Lys Ser Pro His Glu Gly Tyr Glu Val Leu Lys
200 165 170 175
202 ttc gac gac gtg gtc acc aat ctt ggc aat cac tac gac ccc act aca 576
203 Phe Asp Asp Val Val Thr Asn Leu Gly Asn His Tyr Asp Pro Thr Thr
204 180 185 190
206 ggc aag ttc agc tgc cag gtg cgg ggc atc tac ttc ttc acg tac cac 624
207 Gly Lys Phe Ser Cys Gln Val Arg Gly Ile Tyr Phe Phe Thr Tyr His
208 195 200 205
210 att ctc atg cgt ggc ggc gac gga acc agc atg tgg gcg gat ctc tgc 672
211 Ile Leu Met Arg Gly Gly Asp Gly Thr Ser Met Trp Ala Asp Leu Cys
212 210 215 220
214 aag aac ggg cag gtg cga gcc agc gcc ata gcc cag gac gcg gac cag 720
215 Lys Asn Gly Gln Val Arg Ala Ser Ala Ile Ala Gln Asp Ala Asp Gln
216 225 230 235 240
218 aat tac gac tac gcc agc aac agc gtg gta ctg cac ctg gat tca ggc 768
219 Asn Tyr Asp Tyr Ala Ser Asn Ser Val Val Leu His Leu Asp Ser Gly
220 245 250 255
222 gat gaa gtc tac gtg aag ctg gac ggc ggg aag gct cac ggc ggc aac 816
223 Asp Glu Val Tyr Val Lys Leu Asp Gly Gly Lys Ala His Gly Gly Asn
224 260 265 270
226 aat aac aag tac agc acg ttc tcg ggc ttc ctc ctg tat ccg gat tag 864
227 Asn Asn Lys Tyr Ser Thr Phe Ser Gly Phe Leu Leu Tyr Pro Asp *
228 275 280 285
232 <210> SEQ ID NO: 4
233 <211> LENGTH: 287
234 <212> TYPE: PRT
235 <213> ORGANISM: Homo sapiens
237 <400> SEQUENCE: 4
238 Met Ala Leu Gly Leu Leu Ile Ala Val Pro Leu Leu Leu Gln Ala Ala
239 1 5 10 15
240 Pro Pro Gly Ala Ala His Tyr Glu Met Leu Gly Thr Cys Arg Met Ile
241 20 25 30
242 Cys Asp Pro Tyr Ser Val Ala Pro Ala Gly Gly Pro Ala Gly Ala Lys
243 35 40 45
244 Ala Pro Pro Pro Gly Pro Ser Thr Ala Ala Leu Glu Val Met Gln Asp
245 50 55 60

```

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```

246 Leu Ser Ala Asn Pro Pro Pro Phe Ile Gln Gly Pro Lys Gly Asp
247 65 70 75 80
248 Pro Gly Arg Pro Gly Lys Pro Gly Pro Arg Gly Pro Pro Gly Glu Pro
249 85 90 95
250 Gly Pro Pro Gly Pro Arg Gly Pro Pro Gly Glu Lys Gly Asp Ser Gly
251 100 105 110
252 Arg Pro Gly Leu Pro Gly Leu Gln Leu Thr Thr Ser Ala Ala Gly Gly
253 115 120 125
254 Val Gly Val Val Ser Gly Gly Thr Gly Gly Gly Gly Asp Thr Glu Gly
255 130 135 140
256 Glu Val Thr Ser Ala Leu Ser Ala Ala Phe Ser Gly Pro Lys Ile Ala
257 145 150 155 160
258 Phe Tyr Val Gly Leu Lys Ser Pro His Glu Gly Tyr Glu Val Leu Lys
259 165 170 175
260 Phe Asp Asp Val Val Thr Asn Leu Gly Asn His Tyr Asp Pro Thr Thr
261 180 185 190
262 Gly Lys Phe Ser Cys Gln Val Arg Gly Ile Tyr Phe Phe Thr Tyr His
263 195 200 205
264 Ile Leu Met Arg Gly Gly Asp Gly Thr Ser Met Trp Ala Asp Leu Cys
265 210 215 220
266 Lys Asn Gly Gln Val Arg Ala Ser Ala Ile Ala Gln Asp Ala Asp Gln
267 225 230 235 240
268 Asn Tyr Asp Tyr Ala Ser Asn Ser Val Val Leu His Leu Asp Ser Gly
269 245 250 255
270 Asp Glu Val Tyr Val Lys Leu Asp Gly Gly Lys Ala His Gly Gly Asn
271 260 265 270
272 Asn Asn Lys Tyr Ser Thr Phe Ser Gly Phe Leu Leu Tyr Pro Asp
273 275 280 285
276 <210> SEQ ID NO: 5
277 <211> LENGTH: 717
278 <212> TYPE: DNA
279 <213> ORGANISM: Homo sapiens
281 <220> FEATURE:
282 <221> NAME/KEY: CDS
283 <222> LOCATION: (1)...(717)
285 <400> SEQUENCE: 5
286 atg gtg ctg ctg ctg ctg gtg gcc atc ccg ctg ctg gtg cac agc tcc 48
287 Met Val Leu Leu Leu Leu Val Ala Ile Pro Leu Leu Val His Ser Ser
288 1 5 10 15
290 cgc ggg cca gcg cac tac gag atg ctg ggt cgc tgc cgc atg gtg tgc 96
291 Arg Gly Pro Ala His Tyr Glu Met Leu Gly Arg Cys Arg Met Val Cys
292 20 25 30
294 gac ccg cat ggg ccc cgt ggc cct ggt ccc gac ggc gcg cct gct tcc 144
295 Asp Pro His Gly Pro Arg Gly Pro Gly Pro Asp Gly Ala Pro Ala Ser
296 35 40 45
298 gtg ccc ccc ttc ccg cca ggc gcc aag gga gag gtg ggc cgg cgc ggg 192
299 Val Pro Pro Phe Pro Pro Gly Ala Lys Gly Glu Val Gly Arg Arg Gly
300 50 55 60
302 aaa gca ggc ctg cgg ggg ccc cct gga cca cca ggt cca aga ggg ccc 240

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VERIFICATION SUMMARY

DATE: 01/31/2006

PATENT APPLICATION: US/10/510,002

TIME: 15:38:05

Input Set : E:\G-175US03PCT-SEQLIST.txt

Output Set: N:\CRF4\01312006\J510002.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date